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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/811,838

DATE: 04/02/2001

TIME: 11:10:32

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ENTERED

3 <110> APPLICANT: Miller, Duane D.
4 Tigyi, Gabor
5 Dalton, James T.
6 Sardar, Vineet M.
7 Elrod, Don B.
8 Xu, Huiping
9 Baker, Daniel L.
10 Wang, Dean
11 Liliom, Karoly
12 Fischer, David J.
13 Virag, Tamas
14 Nusser, Nora
16 <120> TITLE OF INVENTION: LPA RECEPTOR AGONISTS AND ANTAGONISTS AND METHODS OF
17 USE
19 <130> FILE REFERENCE: 20609/181
C--> 21 <140> CURRENT APPLICATION NUMBER: US/09/811,838
C--> 22 <141> CURRENT FILING DATE: 2001-03-19
24 <150> PRIOR APPLICATION NUMBER: 60/190,370
25 <151> PRIOR FILING DATE: 2000-03-17
27 <160> NUMBER OF SEQ ID NOS: 26
29 <170> SOFTWARE: PatentIn Ver. 2.1
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34 <213> ORGANISM: Homo sapiens
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39 ctgcccacag aatggaacac agtcagcaag ctggtgatgg gacttggaat cactgtttgt 180
40 atcttcatca tgttggccaa cctattgggtc atggtggcaa tctatgtcaa ccgccgcttc 240
41 cattttccta tttattacct aatggctaata ctggctgctg cagacttctt tgctgggttg 300
42 gcctacttct atctcatgtt caacacagga cccaatactc ggagactgac tgttagcaca 360
43 tggctcctgc gtcagggcct cattgacacc agcctgacgg catctgtggc caacttactg 420
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47 ctctacagtg actcttactt agtcttctgg gccattttca acttggtgac ctttgtggta 660
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58 <210> SEQ ID NO: 2
59 <211> LENGTH: 364

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68 20 25 30
70 Phe Tyr Asn Arg Ser Gly Lys His Leu Ala Thr Glu Trp Asn Thr Val
71 35 40 45
73 Ser Lys Leu Val Met Gly Leu Gly Ile Thr Val Cys Ile Phe Ile Met
74 50 55 60
76 Leu Ala Asn Leu Leu Val Met Val Ala Ile Tyr Val Asn Arg Arg Phe
77 65 70 75 80
79 His Phe Pro Ile Tyr Tyr Leu Met Ala Asn Leu Ala Ala Ala Asp Phe
80 85 90 95
82 Phe Ala Gly Leu Ala Tyr Phe Tyr Leu Met Phe Asn Thr Gly Pro Asn
83 100 105 110
85 Thr Arg Arg Leu Thr Val Ser Thr Trp Leu Leu Arg Gln Gly Leu Ile
86 115 120 125
88 Asp Thr Ser Leu Thr Ala Ser Val Ala Asn Leu Leu Ala Ile Ala Ile
89 130 135 140
91 Glu Arg His Ile Thr Val Phe Arg Met Gln Leu His Thr Arg Met Ser
92 145 150 155 160
94 Asn Arg Arg Val Val Val Val Ile Val Val Ile Trp Thr Met Ala Ile
95 165 170 175
97 Val Met Gly Ala Ile Pro Ser Val Gly Trp Asn Cys Ile Cys Asp Ile
98 180 185 190
100 Glu Asn Cys Ser Asn Met Ala Pro Leu Tyr Ser Asp Ser Tyr Leu Val
101 195 200 205
103 Phe Trp Ala Ile Phe Asn Leu Val Thr Phe Val Val Met Val Val Leu
104 210 215 220
106 Tyr Ala His Ile Phe Gly Tyr Val Arg Gln Arg Thr Met Arg Met Ser
107 225 230 235 240
109 Arg His Ser Ser Gly Pro Arg Arg Asn Arg Asp Thr Met Met Ser Leu
110 245 250 255
112 Leu Lys Thr Val Val Ile Val Leu Gly Ala Phe Ile Ile Cys Trp Thr
113 260 265 270
115 Pro Gly Leu Val Leu Leu Leu Leu Asp Val Cys Cys Pro Gln Cys Asp
116 275 280 285
118 Val Leu Ala Tyr Glu Lys Phe Phe Leu Leu Leu Ala Glu Phe Asn Ser
119 290 295 300
121 Ala Met Asn Pro Ile Ile Tyr Ser Tyr Arg Asp Lys Glu Met Ser Ala
122 305 310 315 320
124 Thr Phe Arg Gln Ile Leu Cys Cys Gln Arg Ser Glu Asn Pro Thr Gly
125 325 330 335
127 Pro Thr Glu Ser Ser Asp Arg Ser Ala Ser Ser Leu Asn His Thr Ile
128 340 345 350
130 Leu Ala Gly Val His Ser Asn Asp His Ser Val Val
131 355 360

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141 ggcaaagagc tcagctccca ctggcgggccc aaggatgtgg tcgtggtggc actggggtg 120
142 accgtcagcg tgctggtgct gctgaccaat ctgctgtgca tagcagccat cgcctccaac 180
143 cgccgcttcc accagcccat ctactacctg ctcggaatc tggccgcggc tgacctcttc 240
144 gcgggcgtgg cctacctctt cctcatgttc cacactggtc cccgcacagc ccgactttca 300
145 cttgagggtt ggttctctgc gcagggtctg ctggacacaa gcctcactgc gtcggtggcc 360
146 aactgctggg ccatcgccgt ggagcggcac cgcagtgtga tggccgtgca gctgcacagc 420
147 cgctgcctcc gtggccgcgt ggtcatgttc attgtggcgc tgtgggtggc tgccctgggc 480
148 ctgggggtgc tgcctgcccc ctcttgccac tgcctctgtg ccctggaccg ctgctcacgc 540
149 atggcacccc tgctcagccg ctctatttg gccgtctggg ctctgtcgag cctgcttgtc 600
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151 cgcattggcg agcatgtcag ctgccacccc cgctaccgag agaccacgct cagcctggtc 720
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153 ctgctcctgg atggttttag ctgtgagtcg tgcaatgtcc tggctgtaga aaagtacttc 840
154 ctactgttgg ccgaggccaa ctactgggtc aatgctgctg tgtactcttg ccgagatgct 900
155 gagatgcgcc gcacttcccg ccgcttcttc tgcctgcgct gcctccgcca gtccaccgcg 960
156 gagtctgtcc actatacatc ctctgccag ggaggtgcca gcactcgcat catgcttccc 1020
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169 Tyr Asn Asn Ser Gly Lys Glu Leu Ser Ser His Trp Arg Pro Lys Asp
170 20 25 30
172 Val Val Val Val Ala Leu Gly Leu Thr Val Ser Val Leu Val Leu Leu
173 35 40 45
175 Thr Asn Leu Leu Val Ile Ala Ala Ile Ala Ser Asn Arg Arg Phe His
176 50 55 60
178 Gln Pro Ile Tyr Tyr Leu Leu Gly Asn Leu Ala Ala Ala Asp Leu Phe
179 65 70 75 80
181 Ala Gly Val Ala Tyr Leu Phe Leu Met Phe His Thr Gly Pro Arg Thr
182 85 90 95
184 Ala Arg Leu Ser Leu Glu Gly Trp Phe Leu Arg Gln Gly Leu Leu Asp
185 100 105 110
187 Thr Ser Leu Thr Ala Ser Val Ala Thr Leu Leu Ala Ile Ala Val Glu
188 115 120 125
190 Arg His Arg Ser Val Met Ala Val Gln Leu His Ser Arg Leu Pro Arg
191 130 135 140
193 Gly Arg Val Val Met Leu Ile Val Gly Val Trp Val Ala Ala Leu Gly
194 145 150 155 160
196 Leu Gly Leu Leu Pro Ala His Ser Trp His Cys Leu Cys Ala Leu Asp

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197          165          170          175
199 Arg Cys Ser Arg Met Ala Pro Leu Leu Ser Arg Ser Tyr Leu Ala Val
200          180          185          190
202 Trp Ala Leu Ser Ser Leu Leu Val Phe Leu Leu Met Val Ala Val Tyr
203          195          200          205
205 Thr Arg Ile Phe Phe Tyr Val Arg Arg Arg Val Gln Arg Met Ala Glu
206          210          215          220
208 His Val Ser Cys His Pro Arg Tyr Arg Glu Thr Thr Leu Ser Leu Val
209 225          230          235          240
211 Lys Thr Val Val Ile Ile Leu Gly Ala Phe Val Val Cys Trp Thr Pro
212          245          250          255
214 Gly Gln Val Val Leu Leu Leu Asp Gly Leu Gly Cys Glu Ser Cys Asn
215          260          265          270
217 Val Leu Ala Val Glu Lys Tyr Phe Leu Leu Leu Ala Glu Ala Asn Ser
218          275          280          285
220 Leu Val Asn Ala Ala Val Tyr Ser Cys Arg Asp Ala Glu Met Arg Arg
221          290          295          300
223 Thr Phe Arg Arg Leu Leu Cys Cys Ala Cys Leu Arg Gln Ser Thr Arg
224 305          310          315          320
226 Glu Ser Val His Tyr Thr Ser Ser Ala Gln Gly Gly Ala Ser Thr Arg
227          325          330          335
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236 <213> ORGANISM: Homo sapiens
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240 actgtcgatg actggacagg aacaaagctt gtgattgttt tgtgtgttgg gacgtttttc 120
241 tgccctgttta tttttttttc taattctctg gtcacgcgag cagtgatcaa aaacagaaaa 180
242 ttccatttcc ctttctacta cctgttggct aatttagctg ctgccgattt cttcgctgga 240
243 attgcctatg tattcctgat gtttaacaca ggcccagttt caaaaaacttt gactgtcaac 300
244 cgctggtttc tccgtcaggg gcttctggac agtagcttga ctgcttcctt caccaacttg 360
245 ctgggttatcg ccgtggagag gcacatgtca atcatgagga tgcgggtcca tagcaacctg 420
246 accaaaaaga gggtgacact gctcattttg cttgtctggg ccatcgccat ttttatgggg 480
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249 atcatggttg tgggtgtacct gcggatctac gtgtacgtca agaggaaaac caacgtcttg 660
250 tctccgcata caagtgggtc catcagccgc cggaggacac ccatgaagct aatgaagacg 720
251 gtgatgactg tcttaggggc gtttgtggta tgctggaccc cgggcctggt ggttctgctc 780
252 ctcgacggcc tgaactgcag gcagtgtggc gtgcagcatg tgaaaagggt gttcctgctg 840
253 ctggcgctgc tcaactccgt cgtgaacccc atcatctact cctacaagga cgaggacatg 900
254 tatggcacca tgaagaagat gatctgctgc ttctctcagg agaaccaga gaggcgtccc 960
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260 <211> LENGTH: 353
261 <212> TYPE: PRT

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262 <213> ORGANISM: Homo sapiens

264 <400> SEQUENCE: 6

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268 Ser Asn Thr Asp Thr Val Asp Asp Trp Thr Gly Thr Lys Leu Val Ile
269           20           25           30
271 Val Leu Cys Val Gly Thr Phe Phe Cys Leu Phe Ile Phe Phe Ser Asn
272           35           40           45
274 Ser Leu Val Ile Ala Ala Val Ile Lys Asn Arg Lys Phe His Phe Pro
275           50           55           60
277 Phe Tyr Tyr Leu Leu Ala Asn Leu Ala Ala Ala Asp Phe Phe Ala Gly
278           65           70           75           80
280 Ile Ala Tyr Val Phe Leu Met Phe Asn Thr Gly Pro Val Ser Lys Thr
281           85           90           95
283 Leu Thr Val Asn Arg Trp Phe Leu Arg Gln Gly Leu Leu Asp Ser Ser
284           100          105          110
286 Leu Thr Ala Ser Leu Thr Asn Leu Leu Val Ile Ala Val Glu Arg His
287           115          120          125
289 Met Ser Ile Met Arg Met Arg Val His Ser Asn Leu Thr Lys Lys Arg
290           130          135          140
292 Val Thr Leu Leu Ile Leu Leu Val Trp Ala Ile Ala Ile Phe Met Gly
293           145          150          155          160
295 Ala Val Pro Thr Leu Gly Trp Asn Cys Leu Cys Asn Ile Ser Ala Cys
296           165          170          175
298 Ser Ser Leu Ala Pro Ile Tyr Ser Arg Ser Tyr Leu Val Phe Trp Thr
299           180          185          190
301 Val Ser Asn Leu Met Ala Phe Leu Ile Met Val Val Val Tyr Leu Arg
302           195          200          205
304 Ile Tyr Val Tyr Val Lys Arg Lys Thr Asn Val Leu Ser Pro His Thr
305           210          215          220
307 Ser Gly Ser Ile Ser Arg Arg Arg Thr Pro Met Lys Leu Met Lys Thr
308           225          230          235          240
310 Val Met Thr Val Leu Gly Ala Phe Val Val Cys Trp Thr Pro Gly Leu
311           245          250          255
313 Val Val Leu Leu Asp Gly Leu Asn Cys Arg Gln Cys Gly Val Gln
314           260          265          270
316 His Val Lys Arg Trp Phe Leu Leu Leu Ala Leu Leu Asn Ser Val Val
317           275          280          285
319 Asn Pro Ile Ile Tyr Ser Tyr Lys Asp Glu Asp Met Tyr Gly Thr Met
320           290          295          300
322 Lys Lys Met Ile Cys Cys Phe Ser Gln Glu Asn Pro Glu Arg Arg Pro
323           305          310          315          320
325 Ser Arg Ile Pro Ser Thr Val Leu Ser Arg Ser Asp Thr Gly Ser Gln
326           325          330          335
328 Tyr Ile Glu Asp Ser Ile Ser Gln Gly Ala Val Cys Asn Lys Ser Thr
329           340          345          350
331 Ser
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336 <211> LENGTH: 1260

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VERIFICATION SUMMARY DATE: 04/02/2001
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L:22 M:271 C: Current Filing Date differs, Replaced Current Filing Date